

# SEQUENCE LISTING

<110> ROZEN, Rima

<120> cDNA FOR HUMAN METHYLENETETRAHYDROFOLATE  
REDUCTASE AND USES THEREOF

<130> 04844/005005

<150> US 09/592,595

<151> 2000-06-12

<150> US 09/258,928

<151> 1999-03-01

<150> US 08/738,000

<151> 1997-02-12

<150> PCT/CA95/00314

<151> 1995-05-25

<150> GB 9410620.0

<151> 1994-05-26

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2220

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1980)

<400> 1

aat tcc gga gcc atg gtg aac gaa gcc aga gga aac agc agc ctc aac	48
Asn Ser Gly Ala Met Val Asn Glu Ala Arg Gly Asn Ser Ser Leu Asn	
1 5 10 15	

ccc tgc ttg gag ggc agt gcc agc agt ggc agt gag agc tcc aaa gat	96
Pro Cys Leu Glu Gly Ser Ala Ser Ser Gly Ser Glu Ser Ser Lys Asp	
20 25 30	

agt tcg aga tgt tcc acc ccg ggc ctg gac cct gag cgg cat gag aga	144
Ser Ser Arg Cys Ser Thr Pro Gly Leu Asp Pro Glu Arg His Glu Arg	
35 40 45	

ctc cgg gag aag atg agg cgg cga ttg gaa tct ggt gac aag tgg ttc	192
Leu Arg Glu Lys Met Arg Arg Arg Leu Glu Ser Gly Asp Lys Trp Phe	
50 55 60	

tcc ctg gaa ttc ttc cct cct cga act gct gag gga gct gtc aat ctc	240
Ser Leu Glu Phe Phe Pro Pro Arg Thr Ala Glu Gly Ala Val Asn Leu	

65	70	75	80	
atc tca agg ttt gac cgg atg gca gca ggt ggc ccc ctc tac ata gac				288
Ile Ser Arg Phe Asp Arg Met Ala Ala Gly Gly Pro Leu Tyr Ile Asp	85	90	95	
gtg acc tgg cac cca gca ggt gac cct ggc tca gac aag gag acc tcc				336
Val Thr Trp His Pro Ala Gly Asp Pro Gly Ser Asp Lys Glu Thr Ser	100	105	110	
tcc atg atg atc gcc agc acc gcc gtg aac tac tgt ggc ctg gag acc				384
Ser Met Met Ile Ala Ser Thr Ala Val Asn Tyr Cys Gly Leu Glu Thr	115	120	125	
atc ctg cac atg acc tgc tgc cgt cag cgc ctg gag gag atc acg ggc				432
Ile Leu His Met Thr Cys Cys Arg Gln Arg Leu Glu Glu Ile Thr Gly	130	135	140	
cat ctg cac aaa gct aag cag ctg ggc ctg aag aac atc atg gcg ctg				480
His Leu His Lys Ala Lys Gln Leu Gly Leu Lys Asn Ile Met Ala Leu	145	150	155	160
cgg gga gac cca ata ggt gac cag tgg gaa gag gag gag gga ggc ttc				528
Arg Gly Asp Pro Ile Gly Asp Gln Trp Glu Glu Glu Glu Gly Gly Phe	165	170	175	
aac tac gca gtg gac ctg gtg aag cac atc cga agt gag ttt ggt gac				576
Asn Tyr Ala Val Asp Leu Val Lys His Ile Arg Ser Glu Phe Gly Asp	180	185	190	
tac ttt gac atc tgt gtg gca ggt tac ccc aaa ggc cac ccc gaa gca				624
Tyr Phe Asp Ile Cys Val Ala Gly Tyr Pro Lys Gly His Pro Glu Ala	195	200	205	
ggg agc ttt gag gct gac ctg aag cac ttg aag gag aag gtg tct gcg				672
Gly Ser Phe Glu Ala Asp Leu Lys His Leu Lys Glu Lys Val Ser Ala	210	215	220	
gga gcc gat ttc atc atc acg cag ctt ttc ttt gag gct gac aca ttc				720
Gly Ala Asp Phe Ile Ile Thr Gln Leu Phe Phe Glu Ala Asp Thr Phe	225	230	235	240
ttc cgc ttt gtg aag gca tgc acc gac atg ggc atc act tgc ccc atc				768
Phe Arg Phe Val Lys Ala Cys Thr Asp Met Gly Ile Thr Cys Pro Ile	245	250	255	
gtc ccc ggg atc ttt ccc atc cag ggc tac cac tcc ctt cgg cag ctt				816
Val Pro Gly Ile Phe Pro Ile Gln Gly Tyr His Ser Leu Arg Gln Leu	260	265	270	
gtg aag ctg tcc aag ctg gag gtg cca cag gag atc aag gac gtg att				864
Val Lys Leu Ser Lys Leu Glu Val Pro Gln Glu Ile Lys Asp Val Ile	275	280	285	
gag cca atc aaa gac aac gat gct gcc atc cgc aac tat ggc atc gag				912
Glu Pro Ile Lys Asp Asn Asp Ala Ala Ile Arg Asn Tyr Gly Ile Glu	290	295	300	
ctg gcc gtg agc ctg tgc cag gag ctt ctg gcc agt ggc ttg gtg cca				960

Leu	Ala	Val	Ser	Leu	Cys	Gln	Glu	Leu	Leu	Ala	Ser	Gly	Leu	Val	Pro		
305					310					315					320		
ggc	ctc	cac	ttc	tac	acc	ctc	aac	cgc	gag	atg	gct	acc	aca	gag	gtg	1008	
Gly	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Glu	Met	Ala	Thr	Thr	Glu	Val		
				325					330					335			
ctg	aag	cgc	ctg	ggg	atg	tgg	act	gag	gac	ccc	agg	cgt	ccc	cta	ccc	1056	
Leu	Lys	Arg	Leu	Gly	Met	Trp	Thr	Glu	Asp	Pro	Arg	Arg	Pro	Leu	Pro		
			340					345					350				
tgg	gct	ctc	agt	gcc	cac	ccc	aag	cgc	cga	gag	gaa	gat	gta	cgt	ccc	1104	
Trp	Ala	Leu	Ser	Ala	His	Pro	Lys	Arg	Arg	Glu	Glu	Asp	Val	Arg	Pro		
		355					360					365					
atc	ttc	tgg	gcc	tcc	aga	cca	aag	agt	tac	atc	tac	cgt	acc	cag	gag	1152	
Ile	Phe	Trp	Ala	Ser	Arg	Pro	Lys	Ser	Tyr	Ile	Tyr	Arg	Thr	Gln	Glu		
		370				375					380						
tgg	gac	gag	ttc	cct	aac	ggc	cgc	tgg	ggc	aat	tcc	tct	tcc	cct	gcc	1200	
Trp	Asp	Glu	Phe	Pro	Asn	Gly	Arg	Trp	Gly	Asn	Ser	Ser	Ser	Pro	Ala		
		385			390					395					400		
ttt	ggg	gag	ctg	aag	gac	tac	tac	ctc	ttc	tac	ctg	aag	agc	aag	tcc	1248	
Phe	Gly	Glu	Leu	Lys	Asp	Tyr	Tyr	Leu	Phe	Tyr	Leu	Lys	Ser	Lys	Ser		
				405					410					415			
ccc	aag	gag	gag	ctg	ctg	aag	atg	tgg	ggg	gag	gag	ctg	acc	agt	gaa	1296	
Pro	Lys	Glu	Glu	Leu	Leu	Lys	Met	Trp	Gly	Glu	Glu	Leu	Thr	Ser	Glu		
			420					425					430				
gca	agt	gtc	ttt	gaa	gtc	ttt	gtt	ctt	tac	ctc	tcg	gga	gaa	cca	aac	1344	
Ala	Ser	Val	Phe	Glu	Val	Phe	Val	Leu	Tyr	Leu	Ser	Gly	Glu	Pro	Asn		
		435					440					445					
cgg	aat	ggg	cac	aaa	gtg	act	tgc	ctg	ccc	tgg	aac	gat	gag	ccc	ctg	1392	
Arg	Asn	Gly	His	Lys	Val	Thr	Cys	Leu	Pro	Trp	Asn	Asp	Glu	Pro	Leu		
		450				455					460						
gcg	gct	gag	acc	agc	ctg	ctg	aag	gag	gag	ctg	ctg	cgg	gtg	aac	cgc	1440	
Ala	Ala	Glu	Thr	Ser	Leu	Leu	Lys	Glu	Glu	Leu	Leu	Arg	Val	Asn	Arg		
		465			470				475					480			
cag	ggc	atc	ctc	acc	atc	aac	tca	cag	ccc	aac	atc	aac	ggg	aag	ccg	1488	
Gln	Gly	Ile	Leu	Thr	Ile	Asn	Ser	Gln	Pro	Asn	Ile	Asn	Gly	Lys	Pro		
				485					490					495			
tcc	tcc	gac	ccc	atc	gtg	ggc	tgg	ggc	ccc	agc	ggg	ggc	tat	gtc	ttc	1536	
Ser	Ser	Asp	Pro	Ile	Val	Gly	Trp	Gly	Pro	Ser	Gly	Gly	Tyr	Val	Phe		
			500					505					510				
cag	aag	gcc	tac	tta	gag	ttt	ttc	act	tcc	cgc	gag	aca	gcg	gaa	gca	1584	
Gln	Lys	Ala	Tyr	Leu	Glu	Phe	Phe	Thr	Ser	Arg	Glu	Thr	Ala	Glu	Ala		
		515					520					525					
ctt	ctg	caa	gtg	ctg	aag	aag	tac	gag	ctc	cgg	gtt	aat	tac	cac	ctt	1632	
Leu	Leu	Gln	Val	Leu	Lys	Lys	Tyr	Glu	Leu	Arg	Val	Asn	Tyr	His	Leu		
		530				535					540						





595 600 605  
 Ser Arg Thr Ile Ile Gln Tyr Ile His Asp Asn Tyr Phe Leu Val Asn  
 610 615 620  
 Leu Val Asp Asn Asp Phe Pro Leu Asp Asn Cys Leu Trp Gln Val Val  
 625 630 635 640  
 Glu Asp Thr Leu Glu Leu Leu Asn Arg Pro Thr Gln Asn Ala Arg Glu  
 645 650 655  
 Thr Glu Ala Pro  
 660

<210> 3  
 <211> 2219  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (13)...(1983)

<400> 3  
 aattccggag cc atg gtg aac gaa gcc aga gga aac agc agc ctc aac ccc 51  
 Met Val Asn Glu Ala Arg Gly Asn Ser Ser Leu Asn Pro  
 1 5 10  
 tgc ttg gag ggc agt gcc agc agt ggc agt gag agc tcc aaa gat agt 99  
 Cys Leu Glu Gly Ser Ala Ser Ser Gly Ser Glu Ser Ser Lys Asp Ser  
 15 20 25  
 tcg aga tgt tcc acc ccg ggc ctg gac cct gag cgg cat gag aga ctc 147  
 Ser Arg Cys Ser Thr Pro Gly Leu Asp Pro Glu Arg His Glu Arg Leu  
 30 35 40 45  
 cgg gag aag atg agg cgg cga ttg gaa tct ggt gac aag tgg ttc tcc 195  
 Arg Glu Lys Met Arg Arg Arg Leu Glu Ser Gly Asp Lys Trp Phe Ser  
 50 55 60  
 ctg gaa ttc ttc cct cct cga act gct gag gga gct gtc aat ctc atc 243  
 Leu Glu Phe Phe Pro Pro Arg Thr Ala Glu Gly Ala Val Asn Leu Ile  
 65 70 75  
 tca agg ttt gac cgg atg gca gca ggt ggc ccc ctc tac ata gac gtg 291  
 Ser Arg Phe Asp Arg Met Ala Ala Gly Gly Pro Leu Tyr Ile Asp Val  
 80 85 90  
 acc tgg cac cca gca ggt gac cct ggc tca gac aag gag acc tcc tcc 339  
 Thr Trp His Pro Ala Gly Asp Pro Gly Ser Asp Lys Glu Thr Ser Ser  
 95 100 105  
 atg atg atc gcc agc acc gcc gtg aac tac tgt ggc ctg gag acc atc 387  
 Met Met Ile Ala Ser Thr Ala Val Asn Tyr Cys Gly Leu Glu Thr Ile  
 110 115 120 125  
 ctg cac atg acc tgc tgc cgt cag cgc ctg gag gag atc acg ggc cat 435  
 Leu His Met Thr Cys Cys Arg Gln Arg Leu Glu Glu Ile Thr Gly His  
 130 135 140  
 ctg cac aaa gct aag cag ctg ggc ctg aag aac atc atg gcg ctg cgg 483  
 Leu His Lys Ala Lys Gln Leu Gly Leu Lys Asn Ile Met Ala Leu Arg

145	150	155	
gga gac cca ata ggt gac cag tgg gaa gag gag gag gga ggc ttc aac Gly Asp Pro Ile Gly Asp Gln Trp Glu Glu Glu Glu Gly Gly Phe Asn 160 165 170			531
tac gca gtg gac ctg gtg aag cac atc cga agt gag ttt ggt gac tac Tyr Ala Val Asp Leu Val Lys His Ile Arg Ser Glu Phe Gly Asp Tyr 175 180 185			579
ttt gac atc tgt gtg gca ggt tac ccc aaa ggc cac ccc gaa gca ggg Phe Asp Ile Cys Val Ala Gly Tyr Pro Lys Gly His Pro Glu Ala Gly 190 195 200 205			627
agc ttt gag gct gac ctg aag cac ttg aag gag aag gtg tct gcg gga Ser Phe Glu Ala Asp Leu Lys His Leu Lys Glu Lys Val Ser Ala Gly 210 215 220			675
gcc gat ttc atc atc acg cag ctt ttc ttt gag gct gac aca ttc ttc Ala Asp Phe Ile Ile Thr Gln Leu Phe Phe Glu Ala Asp Thr Phe Phe 225 230 235			723
cgc ttt gtg aag gca tgc acc gac atg ggc atc act tgc ccc atc gtc Arg Phe Val Lys Ala Cys Thr Asp Met Gly Ile Thr Cys Pro Ile Val 240 245 250			771
ccc ggg atc ttt ccc atc cag ggc tac cac tcc ctt cgg cag ctt gtg Pro Gly Ile Phe Pro Ile Gln Gly Tyr His Ser Leu Arg Gln Leu Val 255 260 265			819
aag ctg tcc aag ctg gag gtg cca cag gag atc aag gac gtg att gag Lys Leu Ser Lys Leu Glu Val Pro Gln Glu Ile Lys Asp Val Ile Glu 270 275 280 285			867
cca atc aaa gac aac gat gct gcc atc cgc aac tat ggc atc gag ctg Pro Ile Lys Asp Asn Asp Ala Ala Ile Arg Asn Tyr Gly Ile Glu Leu 290 295 300			915
gcc gtg agc ctg tgc cag gag ctt ctg gcc agt ggc ttg gtg cca ggc Ala Val Ser Leu Cys Gln Glu Leu Leu Ala Ser Gly Leu Val Pro Gly 305 310 315			963
ctc cac ttc tac acc ctc aac cgc gag atg gct acc aca gag gtg ctg Leu His Phe Tyr Thr Leu Asn Arg Glu Met Ala Thr Thr Glu Val Leu 320 325 330			1011
aag cgc ctg ggg atg tgg act gag gac ccc agg cgt ccc cta ccc tgg Lys Arg Leu Gly Met Trp Thr Glu Asp Pro Arg Arg Pro Leu Pro Trp 335 340 345			1059
gct ctc agt gcc cac ccc aag cgc cga gag gaa gat gta cgt ccc atc Ala Leu Ser Ala His Pro Lys Arg Arg Glu Glu Asp Val Arg Pro Ile 350 355 360 365			1107
ttc tgg gcc tcc aga cca aag agt tac atc tac cgt acc cag gag tgg Phe Trp Ala Ser Arg Pro Lys Ser Tyr Ile Tyr Arg Thr Gln Glu Trp 370 375 380			1155
gac gag ttc cct aac ggc cgc tgg ggc aat tcc tct tcc cct gcc ttt			1203

Asp	Glu	Phe	Pro	Asn	Gly	Arg	Trp	Gly	Asn	Ser	Ser	Ser	Pro	Ala	Phe		
			385					390					395				
ggg	gag	ctg	aag	gac	tac	tac	ctc	ttc	tac	ctg	aag	agc	aag	tcc	ccc	1251	
Gly	Glu	Leu	Lys	Asp	Tyr	Tyr	Leu	Phe	Tyr	Leu	Lys	Ser	Lys	Ser	Pro		
		400					405					410					
aag	gag	gag	ctg	ctg	aag	atg	tgg	ggg	gag	gag	ctg	acc	agt	gaa	gca	1299	
Lys	Glu	Glu	Leu	Leu	Lys	Met	Trp	Gly	Glu	Glu		Thr	Ser	Glu	Ala		
		415				420					425						
agt	gtc	ttt	gaa	gtc	ttt	gtt	ctt	tac	ctc	tcg	gga	gaa	cca	aac	cgg	1347	
Ser	Val	Phe	Glu	Val	Phe	Val	Leu	Tyr	Leu	Ser	Gly	Glu	Pro	Asn	Arg		
430					435					440					445		
aat	ggt	cac	aaa	gtg	act	tgc	ctg	ccc	tgg	aac	gat	gag	ccc	ctg	gcg	1395	
Asn	Gly	His	Lys	Val	Thr	Cys	Leu	Pro	Trp	Asn	Asp	Glu	Pro	Leu	Ala		
				450					455					460			
gct	gag	acc	agc	ctg	ctg	aag	gag	gag	ctg	ctg	cgg	gtg	aac	cgc	cag	1443	
Ala	Glu	Thr	Ser	Leu	Leu	Lys	Glu	Glu	Leu	Leu	Arg	Val	Asn	Arg	Gln		
			465					470					475				
ggc	atc	ctc	acc	atc	aac	tca	cag	ccc	aac	atc	aac	ggg	aag	ccg	tcc	1491	
Gly	Ile	Leu	Thr	Ile	Asn	Ser	Gln	Pro	Asn	Ile	Asn	Gly	Lys	Pro	Ser		
		480					485					490					
tcc	gac	ccc	atc	gtg	ggc	tgg	ggc	ccc	agc	ggg	ggc	tat	gtc	ttc	cag	1539	
Ser	Asp	Pro	Ile	Val	Gly	Trp	Gly	Pro	Ser	Gly	Gly	Tyr	Val	Phe	Gln		
		495				500					505						
aag	gcc	tac	tta	gag	ttt	ttc	act	tcc	cgc	gag	aca	gcg	gaa	gca	ctt	1587	
Lys	Ala	Tyr	Leu	Glu	Phe	Phe	Thr	Ser	Arg	Glu	Thr	Ala	Glu	Ala	Leu		
510					515					520					525		
ctg	caa	gtg	ctg	aag	aag	tac	gag	ctc	cgg	gtt	aat	tac	cac	ctt	gtc	1635	
Leu	Gln	Val	Leu	Lys	Lys	Tyr	Glu	Leu	Arg	Val	Asn	Tyr	His	Leu	Val		
				530					535					540			
aat	gtg	aag	ggt	gaa	aac	atc	acc	aat	gcc	cct	gaa	ctg	cag	ccg	aat	1683	
Asn	Val	Lys	Gly	Glu	Asn	Ile	Thr	Asn	Ala	Pro	Glu	Leu	Gln	Pro	Asn		
			545					550					555				
gct	gtc	act	tgg	ggc	atc	ttc	cct	ggg	cga	gag	atc	atc	cag	ccc	acc	1731	
Ala	Val	Thr	Trp	Gly	Ile	Phe	Pro	Gly	Arg	Glu	Ile	Ile	Gln	Pro	Thr		
		560					565					570					
gta	gtg	gat	ccc	gtc	agc	ttc	atg	ttc	tgg	aag	gac	gag	gcc	ttt	gcc	1779	
Val	Val	Asp	Pro	Val	Ser	Phe	Met	Phe	Trp	Lys	Asp	Glu	Ala	Phe	Ala		
		575				580					585						
ctg	tgg	att	gag	cgg	tgg	gga	aag	ctg	tat	gag	gag	gag	tcc	ccg	tcc	1827	
Leu	Trp	Ile	Glu	Arg	Trp	Gly	Lys	Leu	Tyr	Glu	Glu	Glu	Ser	Pro	Ser		
590					595					600					605		
cgc	acc	atc	atc	cag	tac	atc	cac	gac	aac	tac	ttc	ctg	gtc	aac	ctg	1875	
Arg	Thr	Ile	Ile	Gln	Tyr	Ile	His	Asp	Asn	Tyr	Phe	Leu	Val	Asn	Leu		
				610					615					620			

gtg gac aat gac ttc cca ctg gac aac tgc ctc tgg cag gtg gtg gaa 1923  
Val Asp Asn Asp Phe Pro Leu Asp Asn Cys Leu Trp Gln Val Val Glu  
625 630 635

gac aca ttg gag ctt ctc aac agg ccc acc cag aat gcg aga gaa acg 1971  
Asp Thr Leu Glu Leu Leu Asn Arg Pro Thr Gln Asn Ala Arg Glu Thr  
640 645 650

gag gct cca tga ccctgcgtcc tgacgccctg cgttggagcc actcctgtcc 2023  
Glu Ala Pro \*  
655

cgcttctctc ctccacagtg ctgcttctct tgggaactcc actctccttc gtgtctctcc 2083  
caccccgcc tccactcccc cacctgacaa tggcagctag actggagtga ggcttccagg 2143  
ctcttctctg acctgagtcg gcccacatg ggaacctagt actctctgct ctaaaaaaaaa 2203  
aaaaaaaaaa ggaatt 2219

<210> 4  
<211> 656  
<212> PRT  
<213> Homo sapiens

<400> 4  
Met Val Asn Glu Ala Arg Gly Asn Ser Ser Leu Asn Pro Cys Leu Glu  
1 5 10 15  
Gly Ser Ala Ser Ser Gly Ser Glu Ser Ser Lys Asp Ser Ser Arg Cys  
20 25 30  
Ser Thr Pro Gly Leu Asp Pro Glu Arg His Glu Arg Leu Arg Glu Lys  
35 40 45  
Met Arg Arg Arg Leu Glu Ser Gly Asp Lys Trp Phe Ser Leu Glu Phe  
50 55 60  
Phe Pro Pro Arg Thr Ala Glu Gly Ala Val Asn Leu Ile Ser Arg Phe  
65 70 75 80  
Asp Arg Met Ala Ala Gly Gly Pro Leu Tyr Ile Asp Val Thr Trp His  
85 90 95  
Pro Ala Gly Asp Pro Gly Ser Asp Lys Glu Thr Ser Ser Met Met Ile  
100 105 110  
Ala Ser Thr Ala Val Asn Tyr Cys Gly Leu Glu Thr Ile Leu His Met  
115 120 125  
Thr Cys Cys Arg Gln Arg Leu Glu Glu Ile Thr Gly His Leu His Lys  
130 135 140  
Ala Lys Gln Leu Gly Leu Lys Asn Ile Met Ala Leu Arg Gly Asp Pro  
145 150 155 160  
Ile Gly Asp Gln Trp Glu Glu Glu Gly Phe Asn Tyr Ala Val  
165 170 175  
Asp Leu Val Lys His Ile Arg Ser Glu Phe Gly Asp Tyr Phe Asp Ile  
180 185 190  
Cys Val Ala Gly Tyr Pro Lys Gly His Pro Glu Ala Gly Ser Phe Glu  
195 200 205  
Ala Asp Leu Lys His Leu Lys Glu Lys Val Ser Ala Gly Ala Asp Phe  
210 215 220  
Ile Ile Thr Gln Leu Phe Phe Glu Ala Asp Thr Phe Phe Arg Phe Val  
225 230 235 240  
Lys Ala Cys Thr Asp Met Gly Ile Thr Cys Pro Ile Val Pro Gly Ile  
245 250 255  
Phe Pro Ile Gln Gly Tyr His Ser Leu Arg Gln Leu Val Lys Leu Ser  
260 265 270  
Lys Leu Glu Val Pro Gln Glu Ile Lys Asp Val Ile Glu Pro Ile Lys  
275 280 285

Asp	Asn	Asp	Ala	Ala	Ile	Arg	Asn	Tyr	Gly	Ile	Glu	Leu	Ala	Val	Ser	290	295	300
Leu	Cys	Gln	Glu	Leu	Leu	Ala	Ser	Gly	Leu	Val	Pro	Gly	Leu	His	Phe	305	310	315
Tyr	Thr	Leu	Asn	Arg	Glu	Met	Ala	Thr	Thr	Glu	Val	Leu	Lys	Arg	Leu	325	330	335
Gly	Met	Trp	Thr	Glu	Asp	Pro	Arg	Arg	Pro	Leu	Pro	Trp	Ala	Leu	Ser	340	345	350
Ala	His	Pro	Lys	Arg	Arg	Glu	Glu	Asp	Val	Arg	Pro	Ile	Phe	Trp	Ala	355	360	365
Ser	Arg	Pro	Lys	Ser	Tyr	Ile	Tyr	Arg	Thr	Gln	Glu	Trp	Asp	Glu	Phe	370	375	380
Pro	Asn	Gly	Arg	Trp	Gly	Asn	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Glu	Leu	385	390	395
Lys	Asp	Tyr	Tyr	Leu	Phe	Tyr	Leu	Lys	Ser	Lys	Ser	Pro	Lys	Glu	Glu	405	410	415
Leu	Leu	Lys	Met	Trp	Gly	Glu	Glu	Leu	Thr	Ser	Glu	Ala	Ser	Val	Phe	420	425	430
Glu	Val	Phe	Val	Leu	Tyr	Leu	Ser	Gly	Glu	Pro	Asn	Arg	Asn	Gly	His	435	440	445
Lys	Val	Thr	Cys	Leu	Pro	Trp	Asn	Asp	Glu	Pro	Leu	Ala	Ala	Glu	Thr	450	455	460
Ser	Leu	Leu	Lys	Glu	Glu	Leu	Leu	Arg	Val	Asn	Arg	Gln	Gly	Ile	Leu	465	470	475
Thr	Ile	Asn	Ser	Gln	Pro	Asn	Ile	Asn	Gly	Lys	Pro	Ser	Ser	Asp	Pro	485	490	495
Ile	Val	Gly	Trp	Gly	Pro	Ser	Gly	Gly	Tyr	Val	Phe	Gln	Lys	Ala	Tyr	500	505	510
Leu	Glu	Phe	Phe	Thr	Ser	Arg	Glu	Thr	Ala	Glu	Ala	Leu	Leu	Gln	Val	515	520	525
Leu	Lys	Lys	Tyr	Glu	Leu	Arg	Val	Asn	Tyr	His	Leu	Val	Asn	Val	Lys	530	535	540
Gly	Glu	Asn	Ile	Thr	Asn	Ala	Pro	Glu	Leu	Gln	Pro	Asn	Ala	Val	Thr	545	550	555
Trp	Gly	Ile	Phe	Pro	Gly	Arg	Glu	Ile	Ile	Gln	Pro	Thr	Val	Val	Asp	565	570	575
Pro	Val	Ser	Phe	Met	Phe	Trp	Lys	Asp	Glu	Ala	Phe	Ala	Leu	Trp	Ile	580	585	590
Glu	Arg	Trp	Gly	Lys	Leu	Tyr	Glu	Glu	Glu	Ser	Pro	Ser	Arg	Thr	Ile	595	600	605
Ile	Gln	Tyr	Ile	His	Asp	Asn	Tyr	Phe	Leu	Val	Asn	Leu	Val	Asp	Asn	610	615	620
Asp	Phe	Pro	Leu	Asp	Asn	Cys	Leu	Trp	Gln	Val	Glu	Asp	Thr	Leu		625	630	635
Glu	Leu	Leu	Asn	Arg	Pro	Thr	Gln	Asn	Ala	Arg	Glu	Thr	Glu	Ala	Pro	645	650	655

<210> 5  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 5  
 agcctcaacc cctgcttgga gg

<210> 6  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 6  
 tgacagtttg ctccccaggc ac 22

<210> 7  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 7  
 tgaaggagaa ggtgtctgcg gga 23

<210> 8  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 8  
 aggacggtgc ggtgagagtg g 21

<210> 9  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 9  
 cactgtgggtt ggcattgatg atg 23

<210> 10  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 10  
 ggctgctctt ggaccctcct c 21

<210> 11  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer  
 <400> 11  
 tgcttccggc tccctctagc c 21

<210> 12  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer  
 <400> 12  
 cctcccgtc ccaagaacaa ag 22

<210> 13  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer  
 <400> 13  
 tgaaggagaa ggtgtctgcg gga 23

<210> 14  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer  
 <400> 14  
 aggacggtgc ggtgagagtg 20

<210> 15  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Primer  
 <400> 15  
 gggaggagct gaccagtga g 21

<210> 16  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Primer

<400> 16

ggggtcaggc caggggcag

19

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 17

ggttctcccg agaggtaaag atc

23

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Primer

<400> 18

ctgggggatgt ggtggcactg c

21